Amendments to the Specification:

Please add the following paragraph on page 8 line 30 of the specification:

Figs. 4 – 11 (including Figs. 4A, 4B, 4C, 4D; 5A, 5B, 5C; 6A, 6B, 6C; 7A, 7B, 7C; 8A, 8B, 8C; 9A, 9B, 9C, 9D; 10A, 10B, 10C; 11A, 11B, 11C) correspond to SEQ ID Nos. 3 to 10, respectively.

Please replace paragraph beginning on page 10 line 4 with the following amended paragraph:

Pantosti et al. [1989] isolated C. difficile from a number of patients with antibiotic-associated diarrhoea, and prepared SLPs from them. Cerquetti et al. [2000] published N-terminal sequences of SLPs from several strains, indicating wide differences between strains. In 2000 the complete DNA sequence of the C. difficile genome was published ~~(available at web address http://www.sanger.ac.uk/Projects/C_difficile/)~~.

Please replace paragraph beginning on page 10 line 17 with the following amended paragraph:

The slpA gene has been sequenced from a number of strains corresponding to different PCR types. The sequences of strains 171500 (PCR type 1)(NCIMB 41081; PHLS R13537), 172450 (PCR type 5)(PHLS R12884), 170324 (PCR type 12) (NCIMB 41080; PHLS R12882), 171448 (PCR type 12) (PHLS R13550), 171862 (PCR type 17) (PHLS R13702), 173644 (PCR type 31) (PHLS R13711), 170444 (PCR type 46) (PHLS R12883) and 170426 (PCR type 92) (PHLS R12871) with translations thereof are given in Figs. 4 – 11 ~~Appendices 1 to 8~~. Substantial variation in nucleotide and predicted amino acid sequence was found between strains of PCR types 1, 5, 12, 17 and 31. The genes from strains of PCR types 46 and 92 are almost identical in sequence to those of PCR type 12. When the DNA sequences of genes of different strains within a PCR type are compared, the sequences are almost if not quite identical, indicating that the potential for variation is not infinite. These

findings are in agreement with serotyping studies [Delme et al., 1986, 1990], and indicate that the production of an effective vaccine based on the slpA product is feasible. In this respect, the present invention includes all variant slpA genes and their products, individually and combined, fragments of them, and their mutants and derivatives.

Please replace paragraph beginning on page 15 line 23 with the following amended paragraph:

These sequences were used to interrogate the C. difficile genome sequence using the TBLASTN programme, which compared our query sequences with those of the genome project ~~(available at web address http://www.sanger.ac.uk/Projects/C_difficile/)~~, translated in all 6 possible reading frames. A nearly identical stretch of sequence was identified when the sequence from strain 1710324 (type 12) was used for interrogation. The same stretch of sequence was picked up with the sequence from strain 171500 (type 1) was used, although the identity was much less strong. Since the homologous sequence belonged to an open reading frame encoding a 719-residue peptide, this result was somewhat surprising. However, when the N-terminal sequences from the higher molecular weight SLP component were later published by Cerquetti et al [2000], it became apparent that they were encoded downstream along the same gene, subsequently identified as slpA, and the reason for the discrepancy in size between the gene and its products became readily apparent.

Please replace paragraph beginning on page 16 line 27 with the following amended paragraph:

The nucleotide sequences of the slpA genes from the two sample strains of C. difficile (PCR types 1 and 12, deposited at the NCIMB) and of several others (PCR types 5, 12, 17, 31, 46 and 92, available from the Anaerobe Reference Unit at the Department of Medical Microbiology and Public Health Laboratory, Cardiff, Wales were obtained. The slpA gene and flanking sequence was amplified by polymerase chain reaction from genomic DNA prepared from C. difficile using a commercial kit (Puregene.RTM.DNA isolation kit for

yeast and Gram positive bacteria, Gentra systems Minneapolis, Minn.). The forward primer (5' ATGGATTATTATAGAGATGTGAG 3') (SEQ ID No. 11), was based on sequence from the genome sequencing project, starting 112 nucleotides upstream from the start of the slpA open reading frame. Two reverse primers were used, depending on the PCR type. A downstream primer (5' CTATTTAAAGTTTTATTAAAACTTATATTAC 3') (SEQ ID No. 12) was used to amplify slpA from PCR types 12, 17, 31, 46 and 92. A reverse primer based on the 3' end of the slpA open reading frame from strain 630 and the subsequent nonsense codon (5' TTACATATCTAATAAATCTTTCATTTTGTTTATAACTG 3') (SEQ ID No. 13) was used to amplify slpA from PCR types 1 and 5. The choice of primer for the latter two PCR types may have resulted in a small number of systematic errors in the nucleotide sequence obtained. PCR was carried out using HotStar.TM. Taq polymerase (Qiagen Ltd., Crawley, West Sussex, UK) according to the manufacturer's instructions. A single fragment of approximately 2 kb was obtained for each strain, which was then cloned into the pBAD/Thio TOPO vector (Invitrogen, Groningen, Netherlands). Inserts were sequenced from both ends by standard procedures in commercial facilities at MWG (Wolverton Mill South, Milton Keynes, UK) and Cambridge University. New primers were designed on the basis of initial sequencing results, enabling sequencing of both strands to be completed (a process known as chromosome walking).

Please replace paragraph beginning on page 17 line 22 with the following amended paragraph:

The results are shown in Figs. 4 to 11 ~~Appendices 1-8~~.

Please replace paragraph beginning on page 17 line 31 with the following amended paragraph:

SEQ ID No. 3 is ~~Appendix 1 shows~~ the open reading frame with translation for slpA from strain 171500 (PCR type 1)~~, SEQ ID No 3~~. Since the reverse primer was based on the 35 nucleotides from the 3' end of the slpA gene, the sequence is not necessarily 100% accurate in this region. However, this part of the gene does not seem to vary greatly from strain to strain.

Please replace paragraph beginning on page 18 line 1 with the following amended paragraph:

SEQ ID No. 4 is ~~Appendix 2 shows~~ the open reading frame with translation for slpA from strain 172450 (PCR type 5)~~, SEQ ID No 4~~. Again, the sequence obtained for the 3' 35 nucleotides is not fully reliable. This gene is considerably smaller than the other slpA genes sequenced, and shows strong sequence divergence from the other PCR types examined.

Please replace paragraph beginning on page 18 line 8 with the following amended paragraph:

SEQ ID No. 5 is ~~Appendix 3 shows~~ the open reading frame with translation for slpA from strain 170324 (PCR type 12)~~, SEQ ID No 5~~. This gene showed a single base difference when compared with the strain used for the genome sequencing project, strain 630, of the same PCR type. The deduced amino acid sequence is identical.

Please replace paragraph beginning on page 18 line 13 with the following amended paragraph:

SEQ ID No 6 is ~~Appendix 4 shows~~ the open reading frame with translation for slpA from strain 171448 (PCR type 12)~~, SEQ ID No 6~~. This gene was almost identical in sequence to that from strain 170324.

Please replace paragraph beginning on page 18 line 17 with the following amended paragraph:

SEQ ID No 7 is ~~Appendix 5 shows~~ the open reading frame with translation for slpA from strain 171862 (PCR type 17)~~, SEQ ID No 7~~.

Please replace paragraph beginning on page 18 line 20 with the following amended paragraph:

SEQ ID No. 8 is ~~Appendix 6 shows~~ the open reading frame with translation for slpA from strain 173644 (PCR type 31)~~, SEQ ID No 8~~. Like the slpA from strain 172450, this sequence is very dissimilar to those of slpA genes from other PCR types encountered.

Please replace paragraph beginning on page 18 line 25 with the following amended paragraph:

SEQ ID No 9 is ~~Appendix 7 shows~~ the open reading frame with translation for slpA from strain 170444 (PCR type 46)~~, SEQ ID No 9~~. This sequence is virtually identical to that obtained for slpA from PCR type 12 and 92 strains.

Please replace paragraph beginning on page 18 line 29 with the following amended paragraph:

SEQ ID No. 10 ~~Appendix 8 shows~~ the open reading frame with translation for slpA from strain 170426 (PCR type 92)~~, SEQ ID No 10~~. This sequence is virtually identical to that obtained for slpA from PCR type 12 and 46.

Please delete the Appendix 1 – 8 from page 26 through page 57 of the specification. These Appendix 1 – 8 have been reproduced as Figs. 4 – 11 as currently presented.